

BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (238 letters)

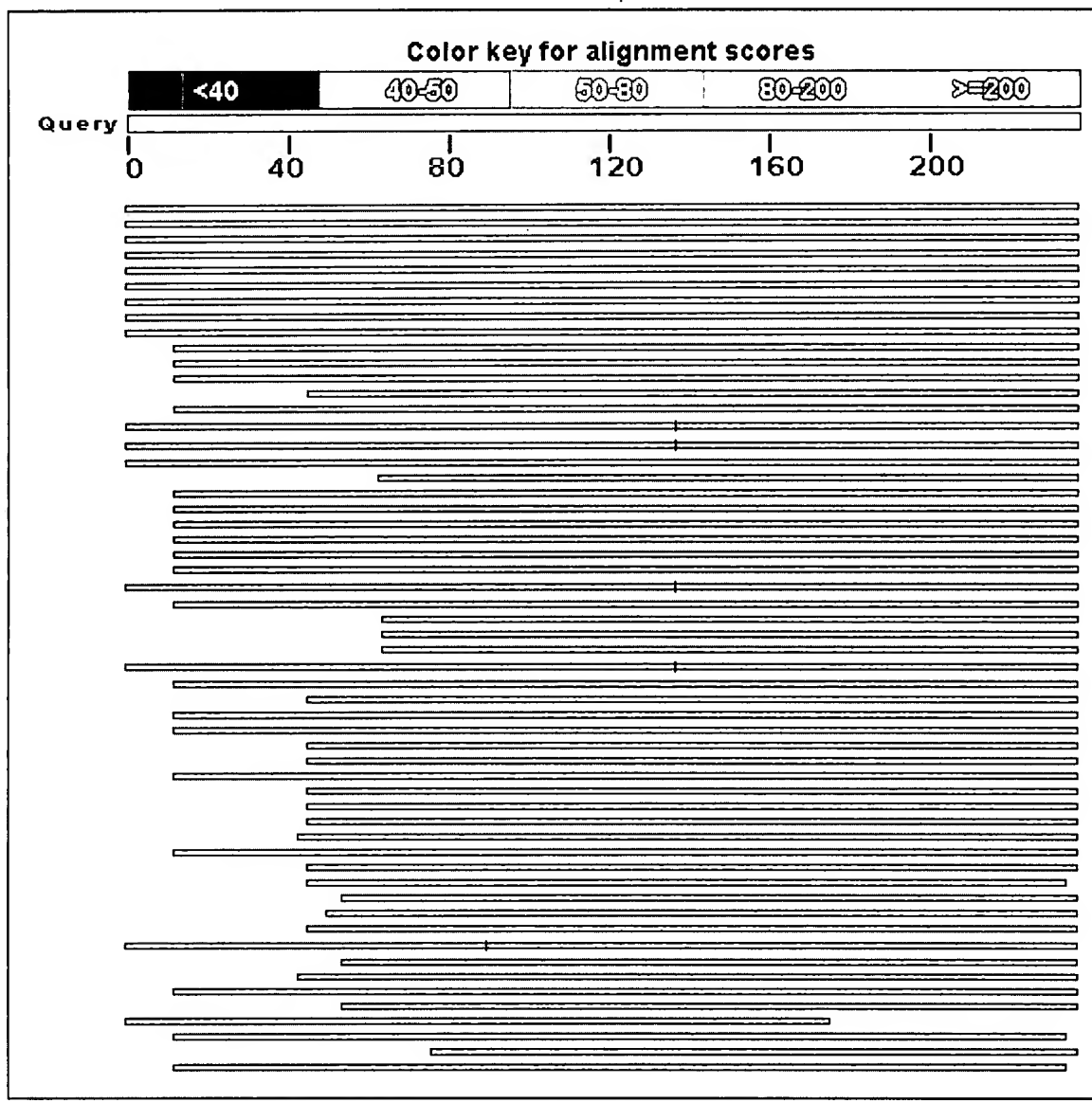
32

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BLASTN 2.2.16 (Mar-25-2007)

RID: 7ZDFWYZJ014 **Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
5,413,143 sequences; 20,916,285,690 total letters

Query= Length=238

*bases 7756 - 7793 of SEQ ID NO:2 (3' UTR of HCV1a)***Distribution of 105 Blast Hits on the Query Sequence**

Distance tree of results **NEW**

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Struct

Sequences producing significant alignments:

(Click headers to sort columns)

AF271632.1	Hepatitis C virus polyprotein gene, complete cds	318	318	100%	5e-84	90%	
AF009072.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #74	316	316	100%	2e-83	90%	
AF177040.1	Synthetic construct clone pH77(p7)-J6S hepatitis C virus, complete genome	300	300	100%	2e-78	90%	
AF177039.1	Synthetic construct clone pH77-J6S hepatitis C virus, complete genome	300	300	100%	2e-78	90%	
AF177038.1	Synthetic construct clone pH77(p7)CV-J6S hepatitis C virus, complete genome	300	300	100%	2e-78	90%	
AF177037.1	Synthetic construct clone pH77CV-J6S hepatitis C virus, complete genome	300	300	100%	2e-78	90%	
AF011753.1	Hepatitis C virus strain H77 pH21 polyprotein gene, complete cds	300	300	100%	2e-78	90%	
AF011752.1	Hepatitis C virus strain H77 pCV-H11 polyprotein gene, complete cds	300	300	100%	2e-78	90%	
AF011751.1	Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds	300	300	100%	2e-78	90%	
AY045702.1	Hepatitis C virus isolate HCR6, complete genome	296	296	94%	2e-77	90%	
AF139594.2	Hepatitis C virus strain HCV-N, complete genome	294	294	94%	8e-77	90%	
AB119282.1	Hepatitis C virus gene for Fusion protein, Feo, complete cds	289	289	94%	4e-75	90%	
D84265.2	Hepatitis C virus (isolate VN004) genomic RNA, complete genome	272	272	81%	4e-70	92%	
AB049089.1	Hepatitis C virus gene for polyprotein, complete cds, isolate:HCVT109	272	272	94%	4e-70	88%	
AF387806.1	Synthetic construct HCV type 1a polyprotein mRNA, complete cds	270	426	100%	1e-69	91%	
AF009606.1	Hepatitis C virus polyprotein gene, complete cds	270	426	100%	1e-69	91%	G
AF009070.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #8	270	270	100%	1e-69	88%	
AF333324.1	Hepatitis C virus type 1b polyprotein mRNA, complete cds	267	267	73%	2e-68	94%	
AF356827.1	Hepatitis C virus isolate HCV-S1, complete genome	263	263	94%	2e-67	87%	
AB049090.1	Hepatitis C virus gene for polyprotein, complete cds, isolate:HCVT140	261	261	94%	8e-67	88%	
D85021.1	Hepatitis C virus genomic RNA for 3'UTR	261	261	94%	8e-67	87%	
AF387808.1	Synthetic construct HCV type 1a/1b chimera mutant polyprotein mRNA, complete cds	259	259	94%	3e-66	88%	
AF387807.1	Synthetic construct HCV type 1a/1b	259	259	94%	3e-	88%	

	chimera polyprotein mRNA, complete cds				66		
AF387805.1	Synthetic construct HCV type 1a/1b chimera polyprotein mRNA, complete cds	259	259	94%	3e-66	88%	
S82227.1	Hepatitis C virus NS5B (NS5B) gene, partial cds	259	415	100%	3e-66	90%	
D63922.1	Hepatitis C virus genomic RNA, 3' UTR	259	259	94%	3e-66	87%	
AF054249.1	Hepatitis C virus HC-J4, pCV-J4L4S, complete genome	259	259	73%	3e-66	93%	
AF054248.1	Hepatitis C virus HC-J4, pCV-J4L2S, complete genome	259	259	73%	3e-66	93%	
AF054247.1	Hepatitis C virus HC-J4, pCV-J4L6S, complete genome	259	259	73%	3e-66	93%	
AF009071.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #10	259	415	100%	3e-66	90%	
AB049088.1	Hepatitis C virus genomic RNA, complete genome, isolate:HCVT094	257	257	94%	1e-65	87%	
D84263.2	Hepatitis C virus (isolate VN235) genomic RNA, complete genome	255	255	81%	4e-65	90%	
D67094.1	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: #12	255	255	94%	4e-65	87%	
AF176573.1	Hepatitis C virus polyprotein precursor, gene, complete cds	254	254	94%	1e-64	87%	
AB049101.1	Hepatitis C virus gene for polyprotein, complete cds, isolate:HCVT221	254	254	81%	1e-64	90%	
AF009076.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #27	254	254	81%	1e-64	90%	
D85020.1	Hepatitis C virus genomic RNA for 3'UTR	254	254	94%	1e-64	87%	
AB049095.1	Hepatitis C virus gene for polyprotein, complete cds, isolate:HCVT169	252	252	81%	5e-64	90%	
AB049091.1	Hepatitis C virus gene for polyprotein, complete cds, isolate:HCVT142	250	250	81%	2e-63	90%	
AB047645.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-6	250	250	81%	2e-63	89%	
D85025.1	Hepatitis C virus genomic RNA for 3'UTR	248	248	81%	6e-63	90%	
D85022.1	Hepatitis C virus genomic RNA for 3'UTR	246	246	94%	2e-62	86%	
AF169003.1	Hepatitis C virus isolate G2aK1 polyprotein gene, complete cds	243	243	81%	3e-61	89%	
AF009075.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16	243	243	79%	3e-61	89%	
D85024.1	Hepatitis C virus genomic RNA for 3'UTR	243	243	77%	3e-61	90%	
D67092.1	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: #6	243	243	78%	3e-61	90%	
AF177036.1	Hepatitis C virus clone pJ6CF, complete genome	241	241	81%	1e-60	89%	
AF009069.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial	241	340	100%	1e-60	94%	

sequence. clone #1.2

AB191333.1	Hepatitis C virus genomic RNA, complete genome, strain:0	239	239	77%	4e-60	90%
D84264.2	Hepatitis C virus (isolate VN405) genomic RNA, complete genome	239	239	81%	4e-60	89%
AJ278830.1	Hepatitis C virus genomic RNA for polyprotein gene	239	239	94%	4e-60	86%
AB080299.1	Hepatitis C virus genomic RNA, complete genome, isolate:M1LE	239	239	77%	4e-60	90%
AF009073.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #5	239	239	73%	4e-60	91%
DQ071885.1	Hepatitis C virus polyprotein mRNA, complete cds	237	237	93%	1e-59	86%
AY460204.1	Hepatitis C virus from Shanghai, complete genome	237	237	68%	1e-59	93%
AJ238799.1	Hepatitis C virus type 1b complete genome, isolate Con1	237	237	93%	1e-59	86%
AJ242651.1	Hepatitis C virus replicon I377/NS2-3'UTR	237	237	93%	1e-59	86%
AJ242654.1	Hepatitis C virus replicon I389/NS3-3'UTR	237	237	93%	1e-59	86%
AJ242653.1	Hepatitis C virus replicon I389/NS2-3'UTR	237	237	93%	1e-59	86%
AJ242652.1	Hepatitis C virus replicon I377/NS3-3'UTR	237	237	93%	1e-59	86%
AF009074.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19	237	237	73%	1e-59	91%
D85023.1	Hepatitis C virus genomic RNA for 3'UTR	237	237	73%	1e-59	91%
D85018.1	Hepatitis C virus genomic RNA for 3'UTR	235	235	73%	5e-59	91%
D67091.1	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: 1090CONS	235	235	69%	5e-59	92%
D84262.2	Hepatitis C virus (isolate Th580) genomic RNA, complete genome	231	231	81%	6e-58	88%
AB047644.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-5	230	230	81%	2e-57	88%
D85019.1	Hepatitis C virus genomic RNA for 3'UTR	230	230	73%	2e-57	91%
D85016.1	Hepatitis C virus genomic RNA for 3'UTR	230	230	73%	2e-57	91%
AF169005.1	Hepatitis C virus isolate NDM59 polyprotein gene, complete cds	228	228	81%	8e-57	88%
D85017.1	Hepatitis C virus genomic RNA for 3'UTR	228	228	72%	8e-57	91%
AF169002.1	Hepatitis C virus isolate NDM228 polyprotein gene, complete cds	226	226	78%	3e-56	89%
D85026.1	Hepatitis C virus genomic RNA for 3'UTR	226	226	81%	3e-56	88%
D67096.1	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: 72CONS	226	226	80%	3e-56	88%
AB237837.1	Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complete sequence	224	224	81%	1e-55	87%

AB047639.1	Hepatitis C virus (isolate JFH-1) genomic RNA, complete genome	224	224	81%	1e- 55	87%
AB114136.1	Hepatitis C virus replicon pSGR-JFH1 gene for neomycin resistance gene product, hepatitis C virus nonstructural protein, complete cds	224	224	81%	1e- 55	87%
D67095.1	Hepatitis C virus genomic RNA, 3'terminus sequence	219	219	72%	5e- 54	89%
AB030907.1	Hepatitis C virus (isolate JPUT971017) genomic RNA, complete genome	217	217	73%	2e- 53	89%
AY746460.1	Hepatitis C virus genotype 2a polyprotein gene, complete cds	215	215	81%	6e- 53	87%
AF169004.1	Hepatitis C virus isolate G2aK3 polyprotein gene, complete cds	215	215	73%	6e- 53	89%
AB047640.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-1	215	215	81%	6e- 53	87%
AB047642.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-3	206	206	82%	4e- 50	85%
AB047641.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-2	206	206	71%	4e- 50	88%
D67093.1	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: #9	202	202	63%	5e- 49	92%
AF009077.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #23	198	198	62%	7e- 48	91%
AB047643.1	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-4	193	193	65%	3e- 46	88%
AB001040.1	Hepatitis C virus (subtype:1b) genomic RNA for polyprotein and 3'UTR, partial cds	193	193	51%	3e- 46	95%
AB016785.1	Hepatitis C virus genomic RNA, complete sequence	191	191	48%	1e- 45	96%
D89815.1	Hepatitis C virus genomic RNA, complete sequence	189	189	58%	4e- 45	91%
D85516.1	Hepatitis C virus genomic RNA, complete cds	187	187	51%	1e- 44	94%
AJ132997.1	Hepatitis C virus, complete genome, isolate HCV-AD78P1	183	183	52%	2e- 43	92%
DQ321850.1	Hepatitis C virus isolate plasma X clone 20 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321849.1	Hepatitis C virus isolate plasma X clone 19 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321848.1	Hepatitis C virus isolate plasma X clone 18 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321847.1	Hepatitis C virus isolate plasma X clone 17 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321846.1	Hepatitis C virus isolate plasma X clone 16 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321845.1	Hepatitis C virus isolate plasma X clone 15 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321844.1	Hepatitis C virus isolate plasma X clone 14 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321843.1	Hepatitis C virus isolate plasma X clone 13 X-tail 3' UTR	176	176	41%	3e- 41	98%
DQ321842.1	Hepatitis C virus isolate plasma X clone 12 X-tail 3' UTR	176	176	41%	3e- 41	98%

Alignments

>gb|AF271632.1|AF271632 Hepatitis C virus polyprotein gene, complete cds
Length=9618

Score = 318 bits (172), Expect = 5e-84
Identities = 223/246 (90%), Gaps = 10/246 (4%)
Strand=Plus/Plus

```

Query 1   TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCC--TCTCttttttttgtt-t
Sbjct 9375 .....TG.T.T.....T..G.

Query 58  ttttgggtttttttgtttttttttttttttttttttttttttttttttttttcctt-c-ttc
Sbjct 9435 ....TTT.....T.....T.....T.....TT..C.T...

Query 116 c-tttttctttttttt--cttctttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAG
Sbjct 9495 .T....T.T.....CC...-...-.....

Query 173 CTGTGAAAGGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGA
Sbjct 9553 .....

Query 233 TCATGT 238
Sbjct 9613 ..... 9618

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>gb|AF009072.1|AF009072 Hepatitis C virus genomic RNA, 3' nontranslated r
sequence. clone #74
Length=321

Score = 316 bits (171), Expect = 2e-83
Identities = 222/244 (90%), Gaps = 13/244 (5%)
Strand=Plus/Plus

```

Query 1   TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCTCTCttttttttgtttttt 6
Sbjct 85 .....-...-G.....-..... 1

Query 61  tgggtttttttgtttttttttttttttttttttttttttttttttttttt-tttccttcttctt 1
Sbjct 141 .CCC.....-.....-.....-...C.....TT... 1

Query 120 t-c--tctttt--tttcttctttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCT 1
Sbjct 198 .C.TT.....CC..C..... 2

Query 175 GTGAAAGGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATC 2
Sbjct 258 .....G.....T.... 3

Query 235 ATGT 238
Sbjct 318 .... 321

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>gb|AF177040.1| Synthetic construct clone pH77(p7)-J6S hepatitis C virus,
genome
Length=9611

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

```

Query 1   TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCTCTCttttttttgtttttt
Sbjct 9387 .....A.....G.-.....-.....

Query 61  tgggtttttttgttttttttttttttttttttttttttttttttttttttcttcttcttctt
Sbjct 9445 .---.....-.....C.-.....C...CC...C...C...---.....

Query 121 ctcttttttttcttcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA
Sbjct 9495 -.....CC.....

Query 181 GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT 23
Sbjct 9554 ..... 96

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>gb|AF177039.1| Synthetic construct clone pH77-J6S hepatitis C virus, comp
genome
Length=9611

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCCTCTCtttttttggttttt	
Sbjct	9387 A G . - -	
Query	61	tgggtttttttgtttttttctttttttttttttttttttttttttttttcatttcttcatttt	
Sbjct	9445	. --- - . . . C . - C . . CC . . C . . C . . -- . - . . . -- . .	
Query	121	ctcttttttttcttctttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA	
Sbjct	9495	- CC	
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	23
Sbjct	9554	96

>gb|AF177038.1| Synthetic construct clone pH77(p7)CV-J6S hepatitis C virus
genome
Length=9611

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTCCTCTCtttttttggttttt
Sbjct	9387A.....G.-.....-.....
Query	61	tgggtttttttgttttttttttttttttttttttttttttttttttttttttttttcattcttcctttt
Sbjct	9445	.---.....-.....C..-.....C...CC...C...C...--.-.....--..
Query	121	ctcttttttttcttcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA
Sbjct	9495	-.....CC.....
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT
Sbjct	9554

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>gb|AF177037.1| Synthetic construct clone pH77CV-J6S hepatitis C virus, co
genome
Length=9611
```

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCTCTCttttttttgtttttt	
Sbjct	9387A.....G.-.....-.....	
Query	61	tgggtttttttgttttttttttttttttttttttttttttttttttttttttttttttttttttt	
Sbjct	9445	.---.....-.....C.-.....C...CC...C...C...--.-.....--..	
Query	121	ctctttttttttctcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA	
Sbjct	9495	-.....CC.....	
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	23
Sbjct	9554	96

>gb|AF011753.1|AF011753 Hepatitis C virus strain H77 pH21 polyprotein gene
cds
Length=9599

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCCCTCTCttttttttgtttttt	
Sbjct	9375A.....G.-.....-.....	
Query	61	tgggtttttttgttttttttttttttttttttttttttttttttttttttttttttttttttt	
Sbjct	9433	.---.....-.....C.-.....C...CC...C...C...--.-.....--..	
Query	121	cttttttttttttttttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA	
Sbjct	9483	-.....CC.....	
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	23
Sbjct	9542	95

>qb|AF011752.1|AF011752 Hepatitis C virus strain H77 pCV-H11 polyprotein g

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cds
Length=9599
```

Score = 300 bits (162), Expect = 2e-78
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCCCTCTCtttttttttgtttttt	
Sbjct	9375A.....G.-.....-.....	
Query	61	tgggtttttttgtttttttttctttttttttttttttttttttcttttttctttctttt	
Sbjct	9433	.---.....-.....C..-.....C...CC...C...C...--.-.....--..	
Query	121	ctcttttttttctttcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA	
Sbjct	9483	-.....CC.....	
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	23
Sbjct	9542	95

>gb|AF011751.1|AF011751 Hepatitis C virus strain H77 pCV-H77C polyprotein
cds
Length=9599

Score = 300 bits (162), Expect = 2e-78 .
Identities = 215/238 (90%), Gaps = 13/238 (5%)
Strand=Plus/Plus

Query	1	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTTCTCTCtttttttttgtttttt	
Sbjct	9375A.....G.-.....-.....	
Query	61	tgggttttttttgttttttttctttttttttttttttttttttttctttctttcttttt	
Sbjct	9433	.---.....-.....C.-.....C...CC...C...C...--.-.....--..	
Query	121	ctcttttttttcttcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA	
Sbjct	9483	-.....CC.....	
Query	181	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	23
Sbjct	9542		95

```
>gb|AY045702.1| Hepatitis C virus isolate HCR6, complete genome
Length=9611
```

Score = 296 bits (160), Expect = 2e-77
Identities = 206/228 (90%), Gaps = 4/228 (1%)
Strand=Plus/Plus

Query	13	TAAACACTCC-GGCCTCTTAGGCCATTTCCCTCTCtttttttgggtttttt
Sbjct	9386A....-AA.....T.T.T.....T.....TTC.....
Query	72	gttttttttcttttttttttttttttttttttttttttccttc-ttccttttctctttttt
Sbjct	9445	T.....T.....T.....T...T..TG....T.T.....
Query	131	cttcttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAAGGTCCGTGAG
Sbjct	9505-T.....
Query	191	CCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT 238
Sbjct	9564 9611

>gb|AF139594.2| Hepatitis C virus strain HCV-N, complete genome
Length=9616

Score = 294 bits (159), Expect = 8e-77
Identities = 209/230 (90%), Gaps = 16/230 (6%)
Strand=Plus/Plus

Query	13	TAAACACTCC-GGCCTCTTAGGCCATTTCTCTCttttttttgtttttttgggttttttt	
Sbjct	9399A....-AA.....-.-.G.....-.....-.-.....	
Query	72	gtttttttttctttttttttttttttttttcttttttcc-tt-cttccttttctctttttt	
Sbjct	9453	-.....-.....-.....-.....T..C...-.....-T.....	
Query	130	t-cttccttttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAGGTCCGTG	
Sbjct	9508	.C.C.....-.....	
Query	189	AGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCATGT	238
Sbjct	9567	9616

WEST Search History

Hide Items Restore Clear Cancel

DATE: Monday, June 25, 2007

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L16	L15 and I9	162
<input type="checkbox"/>	L15	restriction same (subclon\$ or sub adj clon\$4) and substitution with restriction	682
<input type="checkbox"/>	L14	L12 and I10	2
<input type="checkbox"/>	L13	L12 amd I10	16840
<input type="checkbox"/>	L12	I9 and replicon same (virus or viral)	34
<input type="checkbox"/>	L11	I9 and replicon same (HCV or hepatitis adj c)	1
<input type="checkbox"/>	L10	L9 and restriction same (replicon or vector) same (silent)	83
<input type="checkbox"/>	L9	substitution same restriction same (amino adj acid or coding or silent) and (@ad<2000416 or @pd<20020416) and restriction same (replicon or vector)	1014
<input type="checkbox"/>	L8	I6 and substitution same restriction same (amino adj acid or coding or silent)	11
<input type="checkbox"/>	L7	I6 and (@ad<2000416 or @pd<20020416)	2
<input type="checkbox"/>	L6	(HCV or hepatitis adj C) same replicon and replicon same restriction same site	69
<input type="checkbox"/>	L5	(HCV or hepatitis adj C) same replicon and restriction same site	241
<input type="checkbox"/>	L4	L3 and (@ad<2000416 or @pd<20020416)	3
<input type="checkbox"/>	L3	L1 and L2	153
<input type="checkbox"/>	L2	(HCV or hepatitis adj C) same replicon AND (UTR or 3') same (1a or H77)	180
<input type="checkbox"/>	L1	(HCV or hepatitis adj C) same replicon AND (replicon or HCV or virus) same (1a or H77)	223

END OF SEARCH HISTORY